

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Chatterjee, Malaya  
Foon, Kenneth A.  
Chatterjee, Sunil K.

(ii) TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE  
TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA

(iii) NUMBER OF SEQUENCES: 66

(iv) CORRESPONDENCE ADDRESS:

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(E) COUNTRY: USA  
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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US  
(B) FILING DATE:  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Schiff, J. Michael  
(B) REGISTRATION NUMBER: 40,253  
(C) REFERENCE/DOCKET NUMBER: 30414-20002.21

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 447 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..447

5

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide

(B) LOCATION: 58

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

10

ATG AAG TTG CCT GTT AGG CTG TTG GTG CTG ATG TTC TGG ATT CCT GCT	48
Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Ala	
-19 -15 -10 -5	

15

TCC AGC GAT GAT GTT TTC ATG ACC CAA ACT CCA CTC TCC CTG CCT GTC	96
Ser Ser Asp Asp Val Phe Met Thr Gln Thr Pro Leu Ser Leu Pro Val	
1 5 10	

20

AGT CTT GGA GAT CAA GCC TCC ATC TCT TGC AGA TCT AGT CAG AGC ATT	144
Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile	
15 20 25	

25

GTA CAT AGT AAT GGA AAC ACC TAT TTA GAA TGG TAC CTA CAG AAA CCA	192
Val His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro	
30 35 40 45	

30

GGC CAG TCT CCA AAC CTC CTG ATC TAC TTT GTT TCC AAC CGA TTT TCT	240
Gly Gln Ser Pro Asn Leu Leu Ile Tyr Phe Val Ser Asn Arg Phe Ser	
50 55 60	

35

GGG GTC CCA GAC AGG TTC AGT GGC AGT GGA TCA GGG ACA GAT TTC ACA	288
Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr	
65 70 75	

40

CTC AAG ATC AGC AGA GTG GAG GCT GAG GAT CTG GGA GTT TAT TAC TGC	336
Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys	
80 85 90	

45

TTT CAA GGT TCA CAT GTT CCG TGG ACG TTC GGT GGA GGC ACC AAG CTG	384
Phe Gln Gly Ser His Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu	
95 100 105	

GAA ATC AAA CGG GCT GAT GCT GCA CCA ACT GTA TCC ATC TTC CCA CCA	432
Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro	
110 115 120 125	

50

TCC AGT AAG CTT GGG	447
Ser Ser Lys Leu Gly	
130	

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

10 Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Ala  
-19 -15 -10 -5

Ser Ser Asp Asp Val Phe Met Thr Gln Thr Pro Leu Ser Leu Pro Val  
1 5 10

15 Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile  
15 20 25

20 Val His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro  
30 35 40 45

Gly Gln Ser Pro Asn Leu Leu Ile Tyr Phe Val Ser Asn Arg Phe Ser  
50 55 60

25 Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr  
65 70 75

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys  
80 85 90

30 Phe Gln Gly Ser His Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu  
95 100 105

35 Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro  
110 115 120 125

Ser Ser Lys Leu Gly  
130

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..456

126

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide  
(B) LOCATION: 58

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

5	ATG GCT GTC TTG GGG CTG CTC TTC TGC CTG GTG ACA TTC CCA AGC TGT	48
10	Met Ala Val Leu Gly Leu Leu Phe Cys Leu Val Thr Phe Pro Ser Cys	
	-19 -15 -10 -5	
15	GTC CTG TCC CAG GTG CAG GTG AAG GAG TCA GGA CCT TTC CTG GTG CCC	96
	Val Leu Ser Gln Val Gln Val Lys Glu Ser Gly Pro Phe Leu Val Pro	
	1 5 10	
20	CCC TCA CAG AGC CTG TCC ATC ACA TGC ACT GTC TCA GGG TTC TCA TTA	144
	Pro Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu	
	15 20 25	
25	ACC ACC TAT GGT GTA AGC TGG ATT CGC CAG CCT CCA GGA AAG GGT CTG	192
	Thr Thr Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu	
	30 35 40 45	
30	GAG TGG CTG GGA GCA ATT TGG GGT GAC GGG ACC ACA AAT TAT CAT TCA	240
	Glu Trp Leu Gly Ala Ile Trp Gly Asp Gly Thr Thr Asn Tyr His Ser	
	50 55 60	
35	GCT CTC ATA TCC AGA CTG AGC ATC AGC AAG GAT AAC TCC AAG AGC CAA	288
	Ala Leu Ile Ser Arg Leu Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln	
	65 70 75	
40	GTT TTC TTA AAA CTG AAC AGT CTG CAA ACT GAT GAC ACG GCC ACG TAC	336
	Val Phe Leu Lys Leu Asn Ser Leu Gln Thr Asp Asp Thr Ala Thr Tyr	
	80 85 90	
45	TAC TGT GCC AAA CTG GGT AAC TAC GAT GCT CTG GAC TAC TGG GGT CAA	384
	Tyr Cys Ala Lys Leu Gly Asn Tyr Asp Ala Leu Asp Tyr Trp Gly Gln	
	95 100 105	
50	GGA ACC TCA GTC ACC GTC TCC TCA GCC AAA ACG ACA CCC CCA CCC GTC	432
	Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Pro Val	
	110 115 120 125	
55	TAT CCA TTG GTC CCT GGA AGC TTG GG	458
	Tyr Pro Leu Val Pro Gly Ser Leu	
	130	

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids  
(B) TYPE: amino acid

127

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ala Val Leu Gly Leu Leu Phe Cys Leu Val Thr Phe Pro Ser Cys  
-19 -15 -10 -5

10 Val Leu Ser Gln Val Gln Val Lys Glu Ser Gly Pro Phe Leu Val Pro  
1 5 10

15 Pro Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu  
15 20 25

Thr Thr Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu  
30 35 40 45

20 Glu Trp Leu Gly Ala Ile Trp Gly Asp Gly Thr Thr Asn Tyr His Ser  
50 55 60

Ala Leu Ile Ser Arg Leu Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln  
65 70 75

25 Val Phe Leu Lys Leu Asn Ser Leu Gln Thr Asp Asp Thr Ala Thr Tyr  
80 85 90

Tyr Cys Ala Lys Leu Gly Asn Tyr Asp Ala Leu Asp Tyr Trp Gly Gln  
95 100 105

30 Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Pro Val  
110 115 120 125

35 Tyr Pro Leu Val Pro Gly Ser Leu  
130

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 98 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Gln Val Gln Val Lys Glu Ser Gly Pro Phe Leu Val Pro Pro Ser Gln  
1 5 10 15

50 Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Thr Tyr  
20 25 30

Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu  
35 40 45

Gly Ala Ile Trp Gly Asp Gly Thr Thr Asn Tyr His Ser Ala Leu Ile  
50 55 60

Ser Arg Leu Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Leu  
65 70 75 80

Lys Leu Asn Ser Leu Gln Thr Asp Asp Thr Ala Thr Tyr Tyr Cys Ala  
85 90 95

Lys Leu

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Gly Asn Tyr Asp Ala Leu Asp Trp Trp Gly Gln Gly Thr Ser Val Thr  
1 5 10 15

Val Ser Ser

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Tyr Asp Tyr Glu Xaa Xaa Xaa Xaa Xaa  
1 5

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

129

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
1 5

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Ser Val Ser Ile Tyr Tyr Tyr Gly Arg Ser Asp Lys  
1 5 10

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Xaa Xaa Xaa Xaa Xaa Xaa  
1 5

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Xaa Xaa Xaa Xaa  
1

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Arg Asp Tyr Arg  
1

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 5 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Gly Tyr Tyr Asp Xaa  
1 5

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 5 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Xaa Xaa Xaa Xaa Xaa  
1 5

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 112 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly  
1 5 10 15

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile Val His Ser  
20 25 30

Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Lys Gly Gln Ser  
35 40 45



Pro Lys Leu Leu Ile Tyr Phe Val Ser Asn Arg Phe Ser Gly Val Pro  
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile  
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Phe Gln Gly  
85 90 95

Ser His Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys  
100 105 110

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 119 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Gln Val Gln Leu Lys Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln  
1 5 10 15

Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser Tyr  
20 25 30

Gly Val His Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu  
35 40 45

Gly Val Ile Trp Gly Asp Gly Ser Thr Asn Tyr Asn Ser Ala Leu Lys  
50 55 60

Ser Arg Leu Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Leu  
65 70 75 80

Lys Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Arg Tyr Tyr Cys Ala  
85 90 95

Arg Glu Xaa Xaa Xaa Xaa Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly  
100 105 110

Thr Ser Val Thr Val Ser Ser  
115

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 336 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

10 GATGTTTTGA TGACCCAAAC TCCACTCTCC CTGCCTGTCA GTCTTGGAGA TCAAGCCTCC 60  
ATCTCTTGCA GATCTAGTCA GAGCATTGTA CATAGTAATG GAAACACCTA TTTAGAATGG 120  
TACCTGCAGA AACCAGGCCA GTCTCCAAAG CTCCTGATCT ACAAAGTTTC CAACCGATTT 180  
15 TCTGGGGTCC CAGACAGGTT CAGTGGCAGT GGATCAGGGA CAGATTTTAC ACTCAAGATC 240  
AGCAGAGTGG AGGCTGAGGA TCTGGGAGTT TATTACTGCT TTCAAGGTTC ACATGTTCCG 300  
TGGACGTTTCG GTGGAGGCAC CAAGCTGGAA ATCAAA 336

20 (2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:  
25 (A) LENGTH: 336 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

35 GATGTTTTGA TGACCCAAAC TCCACTCTCC CTGCCTGTCA GTCTTGGAGA TCAAGCCTCC 60  
ATCTCTTGCA GATCTAGTCA GAGCATTGTA CATAGTAATG GAAACACCTA TTTAGAATGG 120  
TACCTGCAGA AACCAGGCCA GTCTCCAAAG CTCCTGATCT ACAAAGTTTC CAACCGATTT 180  
40 TCTGGGGTCC CAGACAGGTT CAGTGGCAGT GGATCAGGGA CAGATTTTAC ACTCAAGATC 240  
AGCAGAGTGG AGGCTGAGGA TCTGGGAGTT TATTACTGCT TTCAAGGTTC ACATGTTCCG 300  
TGGACGTTTCG GTGGAGGCAC CAAGCTGGAA ATCAAA 336

45 (2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:  
50 (A) LENGTH: 336 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

5 GATGTTTTGA TGACCCAAAC TCCACTCTCC CTNCCTGTCA GTCTTGGAGA TCAAGCCTCC 60  
ATCTCTTGCA GATCTAGTCA GAGCATTGTA CATAGTAATG GAAACACCTA TTTAGAATGG 120  
10 TACCTGCAGA AACCAGGCCA GTCTCCAAAG CTCCTNATCT ACAAAGTTTC CAACCGATTT 180  
TCTGGGGTCC CAGACAGGTT CAGTGGCAGT GGATCAGGGA CAGATTTTAC ACTCAAGATC 240  
AGCAGAGTGG AGGCTGAGGA TCTGGGAGTT TATTACTGCT TTCAAGGTTC ACATGTTCCG 300  
15 TGGACGTTTC GTGGAGGCAC CAAGCTGGAA ATCAAA 336

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 333 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

30 GATGTTTTGA TGACCCAAAC TCCACTCTCC CTGCCTGTCA GTCTTGGAGA TCAAGCCTCC 60  
ATCTCTTGCA GATCTAGTCA GAGCATTGTA CATAGTAATG GAAACACCTA TTTAGAATGG 120  
TACCTGCAGA AACCAGGCCA GTCTCCAAAG CTCCTGATCT ACAAAGTTTC CAACCGATTT 180  
35 TCTGGGGTCC CAGACAGGTT CAGTGGCAGT GGATCAGGGA CAGATTTTAC ACTCAAGATC 240  
AGCAGAGTGG AGGCTGAGGA TCTGGGAGTT TATTACTGCT TTCAAGGTTC ACATGTTCCG 300  
TGGACGTTTC GTGGAGGCAC CAAGCTGGAA ATC 333

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 336 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GATGTTTTGA TGACCCAAAC TCCACTCTCC CTGCCTGTCA GTCTTGGAGA TCAAGCCTCC 60  
ATCTCTTGCA GATCTAGTCA GAGCATTGTA CATAGTAATG GAAACACCTA TTTAGAATGG 120  
5 TACCTGCAGA AACCAGGCCA GTCTCCAAAG CTCCTGATCT ACAAAGTTTC CAACCGATTT 180  
TCTGGGGTCC CAGACAGGTT CAGTGGCAGT GGATCAGGGA CAGATTTTAC ACTCAAGATC 240  
AGCAGAGTGG AGGCTGAGGA TCTGGGAGTT TATTACTGCT TTCAAGGTTC ACATGTTCCCT 300  
10 CGGACGTTTCG GTGGAGGCAC CAAGCTGGAA ATCAAA 336

(2) INFORMATION FOR SEQ ID NO:22:

- 15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 336 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

25 GATGTTGTGA TGACCCAAAC TCCACTCTCC CTGCCTGTCA GTCTTGGAGA TCAAGCCTCC 60  
ATCTCTTGCA GATCTAGTCA GAGCATTGTA CATAGTAATG GAAACACCTA TTTAGAATGG 120  
30 TACCTGCAGA AGCCAGGCCA GTCTCCAAAG CTCCTGATCT ACAAAGTTTC CAACCGATTT 180  
TCTGGGGTCC CAGACAGGTT CAGTGGCAGT GGATCAGGGA CAGATTTTAC ACTCAAGATC 240  
AGCAGAGTGG AGGCTGAGGA TCTGGGAGTT TATTACTGCT TTCAAGGTTC ACATGTTCCG 300  
35 TGGACGTTTCG GTGGAGGCAC CAAGCTGGAA ATCAAA 336

(2) INFORMATION FOR SEQ ID NO:23:

- 40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 336 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

50 GATGTTTTGA TGACNCAAAC TCCACTCTCC CTGCCTGTCA GTCTTGGAGA TCAAGCCTCC 60  
ATCTCTTGCA GATCTAGTCA GAGCATTGTA CATAGTAATG GAAACACCTA TTTAGAATGG 120

TACCTGCAGA AACCAGGCCA GTCTCCAAAG CTCCTNATCT ACAAAGTTTC CAACCGATTT 180  
TCTGGGGTCC CAGANAGGTT CAGTGGCAGT GGATCAGGGA CAGATTTTCAC ACTCAAGATC 240  
5 AGCAGAGTGG AGGCTGAGGA TCTGGGAGTT TATTACTGCT TTCAAGGTTT ACATGTTCCG 300  
TGGACGTTTCG GTGGAGGCAC CAAGCTGGAA ATCAAA 336

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 333 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

20 GATGTTTTGA TGACCCAAAC TCCACTCTCC CTGCCTGTCA GTCTTGGAGA TCAAGCCTCC 60  
ATCTCTTGCA GATCTAGTCA GAGCATTGTA CATAGTAATG GAAACACCTA TTTAGAATGG 120  
25 TACCTGCAGA AACCAGGCCN GTCTCCAAAG CTCCTGATCT ACAAAGTTTC CAACCGATTT 180  
TCTGGGGTCC CAGACAGGTT CAGTGGCAGT GGATCAGGGA CAGATTTTCAC ACTCAAGATC 240  
AGCAGAGTGG AGGCTGAGGA TCTGGGAGTT TATTACTGCT TTCAAGGTTT ACATGTTCCG 300  
30 TGGACGTTTCG GTGGAGGCAC CAAGCTGGAA ATC 333

(2) INFORMATION FOR SEQ ID NO:25:

- 35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 336 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
40 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

45 GATGTTTTAA TGACCCAAAC TCCACTCTCC CTGCCTGTCA GTCTTGGAGA TCAAGCCTCC 60  
ATCTCTTGCA GATCTAGTCA GAGCATTGTA CATAGTAATG GAAACACCTA TTTAGAATGG 120  
TACCTGCAGA AACCAGGCCA GTCTCCAAAG CTCCTGATCT ACAAAGTTTC CAACCGATTT 180  
50 TCTGGGGTCC CAGACAGGTT CAGTGGCAGT GGATCAGGGA CAGATTTTCAC ACTCAAGATC 240

AGCAGAGTGG AGGCTGAGGA TCTGGGAGTT TATTACTGCT TTCAAGGTTT ACATGTTCCG 300  
TGGACGTTTCG GTGGAGGCAC CAAGCTGGAA ATCAAA 336

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 336 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GATGTTTTGA TGACCCAAAC TCCACTCTCC CTGCCTGTCA GTCTTGGAGA TCAAGCCTCC 60  
ATCTCTTGCA GATCTAGTCA GAGCATTGTA CATAGTAGTG GAAACACCTT TTTAGAATGG 120  
TACCTGCAGA AACCAGGCCA GTCTCCAAAG CTCCTGATCT ACAAAGTTTC CAACCGATTT 180  
TCTGGGGTCC CAGACAGGTT CAGTGGCAGT GGATCAGGGA CAGATTTTAC ACTCAAGATC 240  
AGCAGGGTGG AGGCTGAGGA TCTGGGAGTT TATTACTGCT TTCAAGGTAC ACATGTTCCG 300  
TGGACGTTTCG GTGGAGGCAC CAAGCTGGAA ATCAAA 336

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 291 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CAGGTGCAGC TGCAGGAGTC AGGACCTGGC CTGGTGGCGC CCTCACAGAG CCTGTCCATC 60  
ACATGCACTG TCTCAGGGTT CTCATTAACC AGCTATGGTA TAACCTGGGT TCGCCAGCCT 120  
CCAGGAAAGG GTCTGGAGTG GCTGGGAGTA ATATGGGGTG ACGGAAACAC AAATTATCAT 180  
TCAGCTCTCA TATCCAGACT GAGCATCAGC AAGGATAACT CCAAGAGCCA AGTTTTCTTA 240  
AAACTGAACA GTCTGCAAAC TGATGACACA GCCACGTACT ACTGTGCCAA A 291

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 45 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GCTAAGGACT ACTGGGGTCA AGGAACCTCA GTCACCGTCT CCTCA

45

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 292 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CAGGTGCAGC TGAAGGAGAC AGGACCTGGC CTGGTGGCGC CCTCACAGAG CCTGTCCATC

60

ACATGCACCG TCTCAGGGTT CTCATTAACC AGCTATGGTG TACACTGGGT TCGCCAGCCT

120

CCAGGAAAGG GTCTGGAGTG GCTGGTAGTG ATATGGAGTG ATGGAAGCAC AACTATAAT

180

TCAGCTCTCA AATCCAGACT GAGCATCAGC AAGGACAACT CCAAGAGCCA AGTTTTCTTA

240

AAAATGAACA GTCTCCAAAC TGATGACACA GCCATGTACT ACTGTGCCAG AC

292

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 57 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GGTGACTACT ATGCTATGGA CTACTGGGGT CAAGGAACCT CAGTCACCGT CTCCTCA

57

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 336 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: DNA (genomic) .

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

10 CAGGTGCAGC TGAAGGAGTC AGGACCTGGC CTGGTGGCGC CCTCACAGAG CCTGTCCATC 60  
ACATGCACTG TCTCAGGGTT CTCATTAACC AGCTATGGTG TAAGCTGGGT TCGCCAGCCT 120  
CCAGGAAAGG GTCTGGAGTG GCTGGGAGTA ATATGGGGTG ACGGGAGCAC AAATTATCAT 180  
15 TCAGCTCTCA TATCCAGACT GAGCATCAGC AAGGATAACT CCAAGAGCCA AGTTTTCTTA 240  
AAACTGAACA GTCTGCAAAC TGATGACACA GCCACGTACT ACTGTGCCAA GCATCTTGAC 300  
TACTGGGGCC AAGGCACCAC TCTCACAGTC TCCTCA 336

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 304 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

35 CAGGTGCAGC TGAAGGAGTC AGGACCTGGC CTGGTGGCGC CCTCACAGAG CCTGTCCATC 60  
ACTTGCACTG TCTCTGGGTT TTCATTAACC AGCTATGGTG TAACTGGGT TCGCCAGCCT 120  
CCAGGAAAGG GTCTGGAGTG GCTGGGAGTA ATATGGGCTG GTGGAAGCAC AAATTATAAT 180  
40 TCGGCTCTCA TGTCCAGACT GAGCATCAGC AAAGACAACT CCAAGAGCCA AGTTTTCTTA 240  
AAAATGAACA GTCTGCAAAC TGATGACACA GCCATGTACT ACTGTGCCAG AGGGCATTAC 300  
TACG 304

45 (2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 49 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear



(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

5 CTACTATGCT ATGGACTACT GGGGTCAAGG AACCTCAGTC ACCGTCTCC 49

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 292 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

20 CAGGTGCAGC TCAAGGAGTC AGGACCTGTC CTCGTGGCGC CCTCACAGAG CCTGTCCATC 60  
ACTTGCAGCTG TCTCTGGGTT TTCATTAACC AGCTATGGTG TACTCTGGGT TCGCCAGCCT 120  
CCAGGCAAGG GTCTGGAGTG GCTGGGAGTA ATATGGGCTG GTGGAAGCAC AAATTATAAT 180  
25 TCAGCTCTCA TGTCCAGACT GAGCATCAGC AAAGACAACT CCAAGAGCCA AGTTTCTTA 240  
AAAATGAACA GTCTGCAAAC TGATGACACA GCCATGTACT ACTGTGCCAA AC 292

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
35 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

40 ACAATGCTAT GGACTACTGG GGTCAAGGAA CCTCAGTCAC NGTCTCCTCA 50

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 351 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
50 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

140

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CAGGTNCAGC TGAAGGAGTC AGGACCTGGC CTGGTGGCAC CCTCACAGAG CCTGTCCATC 60  
5 ACATGCACTG TCTCTGGGTT CTCATTATCC AGATATAGTG TACTACTGGGT TCGCCAGCCT 120  
CCAGGAAAGG GTCTTGAGTG GCTGGGAATG ATATGGGGTG GTGGAAACAC AGACTATAAT 180  
10 TCAGCTCTCA AATCCAGACT GAGCATCAGC AAGGACAACT CCAAGAGCCA AGTTTTCTTA 240  
AAAATGAACA GTCTGCAAAC TGATGACACA GCCATGTACT ACTGTGCCAG AGATGGTTAC 300  
TACGACTATG CTATGGACTA CTGGGGTCAA GGAACCTCAG TCACCGTCTC C 351

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CAGGTGCAGC TGAAGGAGTC AGGACCTGGC CTGGTGGCGC CCTCACAGAG CCTGTCCATC 60  
ACTTGCAGT TCTCTGGGTT TTCATTAAACC AGCTATGGTG TACTACTGGGT TCGCCAGCCT 120  
30 CCAGGAAAGG GTCTGGAGTG GCTGGGAGTA ATATGGGCTG GTGGAAGCAC AAATTATAAT 180  
TCGGCTCTCA TGTCCAGACT GAGCATCAGC AAAGACAACT CCAAGAGCCA AGTTTTCTTA 240  
35 AAAATGAACA GTCTGCAAAC TGATGACACA GCCATGTACT ACTGTGCCAG A 291

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TACTATGCTA TGGACTACTG GGGTCAAGGA ACCTCAGTCA CCGTCTCC 48

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CACGTGCACC TGAAGGAGTC AGGACCTGTC CTGGTGGCGC CCTCACAGAG CCTGTCCATC 60  
ACTTGCACTG TCTCTGGGTT TTCATTAACC AACTATGGTG TACTACTGGGT TCGCCAGCCT 120  
CCAGGAAAGG GTCTGGAGTG GCTGGGAGTA ATATGGGCTG GTGGAAACAC AAATTATAAT 180  
TCAGCTCTCA TGTCCAGACT GAGCATCAGC AAAGACAATT CCAAGAGCCA AGTTTCTTA 240  
AAAATGAACA GTCTGCAAAT TGATGACACA GCCATATACT ACTGTGCCAA AC 292

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

TACTATGCTA TGGACTATTG GGGTCAAGGA ACCTCAGTCA CCGTCTCCTC A 51

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CAGGTGCAGC TGAAGGAGTC AGGACCTGGC CTGGTGGCGC CCTCACAGAG CCTGTCCATC 60  
ACTTGCACTG TCTCTGGGTT TCCATTAACC AGCTATGGTG TAGACTGGGT TCGCCAGCCT 120  
CCAGGAAAGG GTCTGGAGTG GCTGGGAGTA ATATGGGGTG GTGGAAGCAC NAATTATAAT 180

TCAGCTCTCA TGTCCAGACT GAGCATCAGC AAAGACAACT CCAAGAGCCA AGTTTTCTTA 240

AAAATGAACA GTCTGCNAAC TGATGACACA GCCATGTACT ACTGTGCC 288

5 (2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ACGGGGNNTT TACTATGCTA TGGACTACTG GGGTCAAGGA ACCTCAGTCA CCGTCTC 57

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CAGGTGCACC TGAAGGAGTC AGGACCTGGC CTGGTGGCGC CCTCACAGAG CCTGTCCATC 60

ACTTGCACTG TCTCTGGATT TTCATTAACC ACCTATGGTG TACACTGGTT TCGCCAGCCT 120

CCAGGAAAGG GTCTGGAGTG GCTGGGACTA ATATGGGCTG GTGGAAACAC AGATTATAAT 180

TCGGCTCTCA TGTCCAGACT GAGCATCAAC AAAGACAACT CCAAGAGCCA AGTTTTCTTA 240

AAAATGAACA GTCTGCAAGC TGATGACACA GCCATGTACT ACTGTGCCAG ATT 293

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

ACGACTATGC TGTGGACTAC TGGGGTCAAG GAACCTCAGT CACCGTCTCC TCA

53

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 30
- (D) OTHER INFORMATION: /note= "N represents the Nucleotide

Inosine(I) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CCCAAGCTTC CAGGGRCCAR KGGATARACN GRTGG

35

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

ACTAGTCGAC ATGGCTGTCY TRGBGCTGYT CYTCTG

36

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

TAATACGACT CACTATAGGG

20

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GTTTTCCCAG TCACGACGT

19

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

ACTAGTCGAC ATGAAGTTGC CTGTTAGGCT GTTGGTGCT

39

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CCCAAGCTTA CTGGATGGTG GGAAGATGGA

30

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

CAGATGGAAG GGCCCAAC

18

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GATTGATGCA TATCATTACC

20

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GTTATCGATG TCGAATAGCC

20

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

TTGCTGCAGA TTGAGTACTG TTCT

24

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GCCGATATCA CCATGGCTGT CTTGGGGCTG CTC

33

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 81 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

TTGGGTCATC AAAACATCGG ATCCGCCGCC ACCCGAGCCG CCACCGCCCG AGCCACCTCC 60  
CCCTGAGGAG ACGGTGACTG A 81

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 81 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

TCAGTCACCG TCTCCTCAGG GGGAGGTGGC TCGGGCGGTG GCGGCTCGGG TGGCGGCGGA 60  
TCCGATGTTT TGATGACCCA A 81

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 34 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

CATCTCTAGA TTATTTGATT TCCAGCTTGG TGCC 34

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GCCGATATCA CCATGGAGTT GCCTGTTAGG CTG 33

(2) INFORMATION FOR SEQ ID NO:61:



(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

TGACTCCTTC ACCTGCACCT GGGATCCGCC GCCACCCGAG CCGCCACCGC CCGAGCCACC 60  
TCCCCCTTTG ATTTCCAGCT TGGTGCC 87

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

GGCACCAAGC TGGAAATCAA AGGGGGAGGT GGCTCGGGCG GTGGCGGCTC GGGTGGCGGC 60  
GGATCCCAGG TGCAGGTGAA GGAGTCA 87

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

CATCTCTAGA TTATGAGGAG ACGGTGACTG AGGT 34

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

ACCATGG 7

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS  
(B) LOCATION: 13..801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

5	GCCGATATCA CC ATG GCT GTC TTG GGG CTG CTC TTC TGC CTG GTG ACA	48
	Met Ala Val Leu Gly Leu Leu Phe Cys Leu Val Thr	
	135 140 145	
10	TTC CCA AGC TGT GTC CTG TCC CAG GTG CAG GTG AAG GAG TCA GGA CCT	96
	Phe Pro Ser Cys Val Leu Ser Gln Val Gln Val Lys Glu Ser Gly Pro	
	150 155 160	
15	TTC CTG GTG CCC CCC TCA CAG AGC CTG TCC ATC ACA TGC ACT GTC TCA	144
	Phe Leu Val Pro Pro Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser	
	165 170 175	
20	GGG TTC TCA TTA ACC ACC TAT GGT GTA AGC TGG ATT CGC CAG CCT CCA	192
	Gly Phe Ser Leu Thr Thr Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro	
	180 185 190	
25	GGA AAG GGT CTG GAG TGG CTG GGA GCA ATT TGG GGT GAC GGG ACC ACA	240
	Gly Lys Gly Leu Glu Trp Leu Gly Ala Ile Trp Gly Asp Gly Thr Thr	
	195 200 205	
30	AAT TAT CAT TCA GCT CTC ATA TCC AGA CTG AGC ATC AGC AAG GAT AAC	288
	Asn Tyr His Ser Ala Leu Ile Ser Arg Leu Ser Ile Ser Lys Asp Asn	
	210 215 220 225	
35	TCC AAG AGC CAA GTT TTC TTA AAA CTG AAC AGT CTG CAA ACT GAT GAC	336
	Ser Lys Ser Gln Val Phe Leu Lys Leu Asn Ser Leu Gln Thr Asp Asp	
	230 235 240	
40	ACG GCC ACG TAC TAC TGT GCC AAA CTG GGT AAC TAC GAT GCT CTG GAC	384
	Thr Ala Thr Tyr Tyr Cys Ala Lys Leu Gly Asn Tyr Asp Ala Leu Asp	
	245 250 255	
45	TAC TGG GGT CAA GGA ACC TCA GTC ACC GTC TCC TCA GGG GGA GGT GGC	432
	Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly Gly	
	260 265 270	
50	TCG GGC GGT GGC GGC TCG GGT GGC GGC GGA TCC GAT GTT TTG ATG ACC	480

149

	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Val	Leu	Met	Thr	
	275						280					285					
5	CAA	ACT	CCA	CTC	TCC	CTG	CCT	GTC	AGT	CTT	GGA	GAT	CAA	GCC	TCC	ATC	528
	Gln	Thr	Pro	Leu	Ser	Leu	Pro	Val	Ser	Leu	Gly	Asp	Gln	Ala	Ser	Ile	
	290					295					300				305		
10	TCT	TGC	AGA	TCT	AGT	CAG	AGC	ATT	GTA	CAT	AGT	AAT	GGA	AAC	ACC	TAT	576
	Ser	Cys	Arg	Ser	Ser	Gln	Ser	Ile	Val	His	Ser	Asn	Gly	Asn	Thr	Tyr	
					310					315					320		
15	TTA	GAA	TGG	TAC	CTA	CAG	AAA	CCA	GGC	CAG	TCT	CCA	AAC	CTC	CTG	ATC	624
	Leu	Glu	Trp	Tyr	Leu	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Asn	Leu	Leu	Ile	
				325					330					335			
20	TAC	TTT	GTT	TCC	AAC	CGA	TTT	TCT	GGG	GTC	CCA	GAC	AGG	TTC	AGT	GGC	672
	Tyr	Phe	Val	Ser	Asn	Arg	Phe	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	
			340					345					350				
25	AGT	GGA	TCA	GGG	ACA	GAT	TTC	ACA	CTC	AAG	ATC	AGC	AGA	GTG	GAG	GCT	720
	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	
		355				360					365						
30	GAG	GAT	CTG	GGA	GTT	TAT	TAC	TGC	TTT	CAA	GGT	TCA	CAT	GTT	CCG	TGG	768
	Glu	Asp	Leu	Gly	Val	Tyr	Tyr	Cys	Phe	Gln	Gly	Ser	His	Val	Pro	Trp	
	370				375					380					385		
35	ACG	TTC	GGT	GGA	GGC	ACC	AAG	CTG	GAA	ATC	AAA	TAATCTAGAG	ATG				814
	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys						
					390					395							

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Met	Ala	Val	Leu	Gly	Leu	Leu	Phe	Cys	Leu	Val	Thr	Phe	Pro	Ser	Cys
1				5					10					15	
Val	Leu	Ser	Gln	Val	Gln	Val	Lys	Glu	Ser	Gly	Pro	Phe	Leu	Val	Pro
			20					25					30		
Pro	Ser	Gln	Ser	Leu	Ser	Ile	Thr	Cys	Thr	Val	Ser	Gly	Phe	Ser	Leu
		35					40					45			
Thr	Thr	Tyr	Gly	Val	Ser	Trp	Ile	Arg	Gln	Pro	Pro	Gly	Lys	Gly	Leu

	50	55	60
5	Glu Trp Leu Gly Ala Ile Trp Gly Asp Gly Thr Thr Asn Tyr His Ser 65 70 75 80		
	Ala Leu Ile Ser Arg Leu Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln 85 90 95		
10	Val Phe Leu Lys Leu Asn Ser Leu Gln Thr Asp Asp Thr Ala Thr Tyr 100 105 110		
	Tyr Cys Ala Lys Leu Gly Asn Tyr Asp Ala Leu Asp Tyr Trp Gly Gln 115 120 125		
15	Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly 130 135 140		
	Gly Ser Gly Gly Gly Gly Ser Asp Val Leu Met Thr Gln Thr Pro Leu 145 150 155 160		
20	Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser 165 170 175		
	Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr 180 185 190		
25	Leu Gln Lys Pro Gly Gln Ser Pro Asn Leu Leu Ile Tyr Phe Val Ser 195 200 205		
30	Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly 210 215 220		
	Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly 225 230 235 240		
35	Val Tyr Tyr Cys Phe Gln Gly Ser His Val Pro Trp Thr Phe Gly Gly 245 250 255		
40	Gly Thr Lys Leu Glu Ile Lys 260		